

Y. PAK

RUSH #12

ENTERED
See page 6

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/913,329A

DATE: 05/22/2003

TIME: 11:10:11

Input Set : A:\EP.txt

Output Set: N:\CRF4\05222003\I913329A.raw

3 <110> APPLICANT: UNIVERSITE DE MONTREAL
 5 <120> TITLE OF INVENTION: NEW METALLOPROTEASES OF THE NEPRILYSIN FAMILY
 7 <130> FILE REFERENCE: BIOMEP INC. NEPRILYSIN
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/913,329A
 C--> 10 <141> CURRENT FILING DATE: 2001-08-21
 12 <150> PRIOR APPLICATION NUMBER: 2,260,376
 13 <151> PRIOR FILING DATE: 1999-02-11
 15 <160> NUMBER OF SEQ ID NOS: 17
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 750
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Homo sapiens
 24 <400> SEQUENCE: 1
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 26 1 5 10 15
 28 Lys Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser
 29 20 25 30
 31 Val Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu
 32 35 40 45
 34 Tyr Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys
 35 50 55 60
 37 Ser Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys
 38 65 70 75 80
 40 Thr Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val
 41 85 90 95
 43 Ile Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp
 44 100 105 110
 46 Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu
 47 115 120 125
 49 Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile
 50 130 135 140
 52 Asn Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu
 53 145 150 155 160
 55 Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln
 56 165 170 175
 58 Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn
 59 180 185 190
 61 Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp
 62 195 200 205
 64 Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu
 65 210 215 220
 67 Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu

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68	225	230	235	240													
70	Ala	Cys	Thr	Ala	Tyr	Val	Asp	Phe	Met	Ile	Ser	Val	Ala	Arg	Leu	Ile	
71					245				250						255		
73	Arg	Gln	Glu	Glu	Arg	Leu	Pro	Ile	Asp	Glu	Asn	Gln	Leu	Ala	Leu	Glu	
74						260			265						270		
76	Met	Asn	Lys	Val	Met	Glu	Leu	Glu	Lys	Glu	Ile	Ala	Asn	Ala	Thr	Ala	
77						275			280						285		
79	Lys	Pro	Glu	Asp	Arg	Asn	Asp	Pro	Met	Leu	Leu	Tyr	Asn	Lys	Met	Thr	
80						290			295						300		
82	Leu	Ala	Gln	Ile	Gln	Asn	Asn	Phe	Ser	Leu	Glu	Ile	Asn	Gly	Lys	Pro	
83	305					310					315					320	
85	Phe	Ser	Trp	Leu	Asn	Phe	Thr	Asn	Glu	Ile	Met	Ser	Thr	Val	Asn	Ile	
86						325			330						335		
88	Ser	Ile	Thr	Asn	Glu	Glu	Asp	Val	Val	Val	Tyr	Ala	Pro	Glu	Tyr	Leu	
89						340			345						350		
91	Thr	Lys	Leu	Lys	Pro	Ile	Leu	Thr	Lys	Tyr	Ser	Ala	Arg	Asp	Leu	Gln	
92						355			360						365		
94	Asn	Leu	Met	Ser	Trp	Arg	Phe	Ile	Met	Asp	Leu	Val	Ser	Ser	Leu	Ser	
95						370			375						380		
97	Arg	Thr	Tyr	Lys	Glu	Ser	Arg	Asn	Ala	Phe	Arg	Lys	Ala	Leu	Tyr	Gly	
98	385					390			395						400		
100	Thr	Thr	Ser	Glu	Thr	Ala	Thr	Trp	Arg	Arg	Cys	Ala	Asn	Tyr	Val	Asn	
101						405			410						415		
103	Gly	Asn	Met	Glu	Asn	Ala	Val	Gly	Arg	Leu	Tyr	Val	Glu	Ala	Ala	Phe	
104						420			425						430		
106	Ala	Gly	Glu	Ser	Lys	His	Val	Val	Glu	Asp	Leu	Ile	Ala	Gln	Ile	Arg	
107						435			440						445		
109	Glu	Val	Phe	Ile	Gln	Thr	Leu	Asp	Asp	Leu	Thr	Trp	Met	Asp	Ala	Glu	
110						450			455						460		
112	Thr	Lys	Lys	Arg	Ala	Glu	Glu	Lys	Ala	Leu	Ile	Lys	Glu	Arg	Ile		
113	465					470			475						480		
115	Gly	Tyr	Pro	Asp	Asp	Ile	Val	Ser	Asn	Asp	Asn	Lys	Leu	Asn	Asn	Glu	
116						485			490						495		
118	Tyr	Leu	Glu	Leu	Asn	Tyr	Lys	Glu	Asp	Glu	Tyr	Phe	Glu	Asn	Ile	Ile	
119						500			505						510		
121	Gln	Asn	Leu	Lys	Phe	Ser	Gln	Ser	Lys	Gln	Leu	Lys	Lys	Leu	Arg	Glu	
122						515			520						525		
124	Lys	Val	Asp	Lys	Asp	Glu	Trp	Ile	Ser	Gly	Ala	Ala	Val	Val	Asn	Ala	
125						530			535						540		
127	Phe	Tyr	Ser	Ser	Gly	Arg	Asn	Gln	Ile	Val	Phe	Pro	Ala	Gly	Ile	Leu	
128	545					550			555						560		
130	Gln	Pro	Pro	Phe	Phe	Ser	Ala	Gln	Gln	Ser	Asn	Ser	Leu	Asn	Tyr	Gly	
131						565			570						575		
133	Gly	Ile	Gly	Met	Val	Ile	Gly	His	Glu	Ile	Thr	His	Gly	Phe	Asp	Asp	
134						580			585						590		
136	Asn	Gly	Arg	Asn	Asn	Phe	Asn	Lys	Asp	Gly	Asp	Leu	Val	Asp	Trp	Trp	Thr
137						595			600						605		
139	Gln	Gln	Ser	Ala	Ser	Asn	Phe	Lys	Glu	Gln	Ser	Gln	Cys	Met	Val	Tyr	
140						610			615						620		

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142 Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His Leu Asn
 143 625 630 635 640
 145 Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Gly
 146 645 650 655
 148 Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr Ile Lys Lys Asn Gly Glu Glu
 149 660 665 670
 151 Lys Leu Leu Pro Gly Leu Asp Leu Asn His Lys Gln Leu Phe Phe Leu
 152 675 680 685
 154 Asn Phe Ala Gln Val Trp Cys Gly Thr Tyr Arg Pro Glu Tyr Ala Val
 155 690 695 700
 157 Asn Ser Ile Lys Thr Asp Val His Ser Pro Gly Asn Phe Arg Ile Ile
 158 705 710 715 720
 160 Gly Thr Leu Gln Asn Ser Ala Glu Phe Ser Glu Ala Phe His Cys Arg
 161 725 730 735
 163 Lys Asn Ser Tyr Met Asn Pro Glu Lys Lys Cys Arg Val Trp
 164 740 745 750
 167 <210> SEQ ID NO: 2
 168 <211> LENGTH: 749
 169 <212> TYPE: PRT
 170 <213> ORGANISM: Homo sapiens
 172 <400> SEQUENCE: 2
 173 Met Glu Ala Glu Thr Gly Ser Ser Val Glu Thr Gly Lys Lys Ala Asn
 174 1 5 10 15
 176 Arg Gly Thr Arg Ile Ala Leu Val Val Phe Val Gly Gly Thr Leu Val
 177 20 25 30
 179 Leu Gly Thr Ile Leu Phe Leu Val Ser Gln Gly Leu Leu Ser Leu Gln
 180 35 40 45
 182 Ala Lys Gln Glu Tyr Cys Leu Lys Pro Glu Cys Ile Glu Ala Ala Ala
 183 50 55 60
 185 Ala Ile Leu Ser Lys Val Asn Leu Ser Val Asp Pro Cys Asp Asn Phe
 186 65 70 75 80
 188 Phe Arg Phe Ala Cys Asp Gly Trp Ile Ser Asn Asn Pro Ile Pro Glu
 189 85 90 95
 191 Asp Met Pro Ser Tyr Gly Val Tyr Pro Trp Leu Arg His Asn Val Asp
 192 100 105 110
 194 Leu Lys Leu Lys Glu Leu Leu Glu Lys Ser Ile Ser Arg Arg Arg Asp
 195 115 120 125
 197 Thr Glu Ala Ile Gln Lys Ala Lys Ile Leu Tyr Ser Ser Cys Met Asn
 198 130 135 140
 200 Glu Lys Ala Ile Glu Lys Ala Asp Ala Lys Pro Leu Leu His Ile Leu
 201 145 150 155 160
 203 Arg His Ser Pro Phe Arg Trp Pro Val Leu Glu Ser Asn Ile Gly Pro
 204 165 170 175
 206 Glu Gly Val Trp Ser Glu Arg Lys Phe Ser Leu Leu Gln Thr Leu Ala
 207 180 185 190
 209 Thr Phe Arg Gly Gln Tyr Ser Asn Ser Val Phe Ile Arg Leu Tyr Val
 210 195 200 205
 212 Ser Pro Asp Asp Lys Ala Ser Asn Glu His Ile Leu Lys Leu Asp Gln
 213 210 215 220

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215 Ala Thr Leu Ser Leu Ala Val Arg Glu Asp Tyr Leu Asp Asn Ser Thr
 216 225 230 235 240
 218 Glu Ala Lys Ser Tyr Arg Asp Ala Leu Tyr Lys Phe Met Val Asp Thr
 219 245 250 255
 221 Ala Val Leu Leu Gly Ala Asn Ser Ser Arg Ala Glu His Asp Met Lys
 222 260 265 270
 224 Ser Val Leu Arg Leu Glu Ile Lys Ile Ala Glu Ile Met Ile Pro His
 225 275 280 285
 227 Glu Asn Arg Thr Ser Glu Ala Met Tyr Asn Lys Met Asn Ile Ser Glu
 228 290 295 300
 230 Leu Ser Ala Met Ile Pro Gln Phe Asp Trp Leu Gly Tyr Ile Lys Lys
 231 305 310 315 320
 233 Val Ile Asp Thr Arg Leu Tyr Pro His Leu Lys Asp Ile Ser Pro Ser
 234 325 330 335
 236 Glu Asn Val Val Val Arg Val Pro Gln Tyr Phe Lys Asp Leu Phe Arg
 237 340 345 350
 239 Ile Leu Gly Ser Glu Arg Lys Lys Thr Ile Ala Asn Tyr Leu Val Trp
 240 355 360 365
 242 Arg Met Val Tyr Ser Arg Ile Pro Asn Leu Ser Arg Arg Phe Gln Tyr
 243 370 375 380
 245 Arg Trp Leu Glu Phe Ser Arg Val Ile Gln Gly Thr Thr Thr Leu Leu
 246 385 390 395 400
 248 Pro Gln Trp Asp Lys Cys Val Asn Phe Ile Glu Ser Ala Leu Pro Tyr
 249 405 410 415
 251 Val Val Gly Lys Met Phe Val Asp Val Tyr Phe Gln Glu Asp Lys Lys
 252 420 425 430
 254 Glu Met Met Glu Glu Leu Val Glu Gly Val Arg Trp Ala Phe Ile Asp
 255 435 440 445
 257 Met Leu Glu Lys Glu Asn Glu Trp Met Asp Ala Gly Thr Lys Arg Lys
 258 450 455 460
 260 Ala Lys Glu Lys Ala Arg Ala Val Leu Ala Lys Val Gly Tyr Pro Glu
 261 465 470 475 480
 263 Phe Ile Met Asn Asp Thr His Val Asn Glu Asp Leu Lys Ala Ile Lys
 264 485 490 495
 266 Phe Ser Glu Ala Asp Tyr Phe Gly Asn Val Leu Gln Thr Arg Lys Tyr
 267 500 505 510
 269 Leu Ala Gln Ser Asp Phe Phe Trp Leu Arg Lys Ala Val Pro Lys Thr
 270 515 520 525
 272 Glu Trp Phe Thr Asn Pro Thr Thr Val Asn Ala Phe Tyr Ser Ala Ser
 273 530 535 540
 275 Thr Asn Gln Ile Arg Phe Pro Ala Gly Glu Leu Gln Lys Pro Phe Phe
 276 545 550 555 560
 278 Trp Gly Thr Glu Tyr Pro Arg Ser Leu Ser Tyr Gly Ala Ile Gly Val
 279 565 570 575
 281 Ile Val Gly His Glu Phe Thr His Gly Phe Asp Asn Asn Gly Arg Lys
 282 580 585 590
 284 Tyr Asp Lys Asn Gly Asn Leu Asp Pro Trp Trp Ser Thr Glu Ser Glu
 285 595 600 605
 287 Glu Lys Phe Lys Glu Lys Thr Lys Cys Met Ile Asn Gln Tyr Ser Asn

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288	610	615	620														
290	Tyr	Tyr	Trp	Lys	Lys	Ala	Gly	Leu	Asn	Val	Lys	Gly	Lys	Arg	Thr	Leu	
291	625			630			635				640						
293	Gly	Glu	Asn	Ile	Ala	Asp	Asn	Gly	Gly	Leu	Arg	Glu	Ala	Phe	Arg	Ala	
294					645				650			655					
296	Tyr	Arg	Lys	Trp	Ile	Asn	Asp	Arg	Arg	Gln	Gly	Leu	Glu	Glu	Pro	Leu	
297					660				665			670					
299	Leu	Pro	Gly	Ile	Thr	Phe	Thr	Asn	Asn	Gln	Leu	Phe	Phe	Leu	Ser	Tyr	
300		675				680				685							
302	Ala	His	Val	Arg	Cys	Asn	Ser	Tyr	Arg	Pro	Glu	Ala	Ala	Arg	Glu	Gln	
303		690				695				700							
305	Val	Gln	Ile	Gly	Ala	His	Ser	Pro	Pro	Gln	Phe	Arg	Val	Asn	Gly	Ala	
306		705				710				715			720				
308	Ile	Ser	Asn	Phe	Glu	Glu	Phe	Gln	Lys	Ala	Phe	Asn	Cys	Pro	Pro	Asn	
309				725					730			735					
311	Ser	Thr	Met	Asn	Arg	Gly	Met	Asp	Ser	Cys	Arg	Leu	Trp				
312			740				745										
315	<210>	SEQ	ID	NO:	3												
316	<211>	LENGTH:	732														
317	<212>	TYPE:	PRT														
318	<213>	ORGANISM:	Homo sapiens														
320	<400>	SEQUENCE:	3														
321	Met	Glu	Gly	Gly	Asp	Gln	Ser	Glu	Glu	Glu	Pro	Arg	Glu	Arg	Ser	Gln	
322	1				5			10			15						
324	Ala	Gly	Gly	Met	Gly	Thr	Leu	Trp	Ser	Gln	Glu	Ser	Thr	Pro	Glu	Glu	
325				20			25			30							
327	Arg	Leu	Pro	Val	Glu	Gly	Ser	Arg	Pro	Trp	Ala	Val	Ala	Arg	Arg	Val	
328		35				40			45								
330	Leu	Thr	Ala	Ile	Leu	Ile	Leu	Gly	Leu	Leu	Leu	Cys	Phe	Ser	Val	Leu	
331		50				55			60								
333	Leu	Phe	Tyr	Asn	Phe	Gln	Asn	Cys	Gly	Pro	Arg	Pro	Cys	Glu	Thr	Ser	
334		65				70			75			80					
336	Val	Cys	Leu	Asp	Leu	Arg	Asp	His	Tyr	Leu	Ala	Ser	Gly	Asn	Thr	Ser	
337			85				90			95							
339	Val	Ala	Pro	Cys	Thr	Asp	Phe	Phe	Ser	Phe	Ala	Cys	Gly	Arg	Ala	Lys	
340		100				105			110								
342	Glu	Thr	Asn	Asn	Ser	Phe	Gln	Glu	Leu	Ala	Thr	Lys	Asn	Lys	Asn	Arg	
343		115				120			125								
345	Leu	Arg	Arg	Ile	Leu	Glu	Val	Gln	Asn	Ser	Trp	His	Pro	Gly	Ser	Gly	
346		130				135			140								
348	Glu	Glu	Lys	Ala	Phe	Gln	Phe	Tyr	Asn	Ser	Cys	Met	Asp	Thr	Leu	Ala	
349		145				150			155			160					
351	Ile	Glu	Ala	Ala	Gly	Thr	Gly	Pro	Leu	Arg	Gln	Val	Ile	Glu	Glu	Leu	
352			165				170			175							
354	Gly	Gly	Trp	Arg	Ile	Ser	Gly	Lys	Trp	Thr	Ser	Leu	Asn	Phe	Asn	Arg	
355			180				185			190							
357	Thr	Leu	Arg	Leu	Leu	Met	Ser	Gln	Tyr	Gly	His	Phe	Pro	Phe	Phe	Arg	
358		195				200			205								
360	Ala	Tyr	Leu	Gly	Pro	His	Pro	Ala	Ser	Pro	His	Thr	Pro	Val	Ile	Gln	

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/913,329A

DATE: 05/22/2003
TIME: 11:10:12

Input Set : A:\EP.txt
Output Set: N:\CRF4\05222003\I913329A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 14,18,21
Seq#:6; N Pos. 14,18,21
Seq#:7; N Pos. 4,7,14,17,20,25
Seq#:8; N Pos. 4,7,14,17,20,25
Seq#:9; N Pos. 2,3,6,9,18,21
Seq#:10; N Pos. 12,24
Seq#:11; N Pos. 9,12,31

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0